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                                         CPAGHTLARPCTEPCGNSTCLVCPQDTFLAWENHHNSECARCQACDEQASQVALENCS
AVADTRACGREGWFVECQVSGSPFYGQPCLDGGALMFRTRLLCSREDTDGGTCL
LGFYEHGDGCVSCPTSTLGSGPSAVGWRQMFWQVLLAGLVYPLLLGATLTTY
RHCWPHYRDLYTADEAGWRALTPPPATHLSPLDSAHTLLAPPDSSEKICTVQLVGNSWT
PGYFETQEALCPQVTWSWDQLPSRALGPAAAPTLSPESPAGSPAWMLQPGPQLTDVWD
RWGLDGCVEDLRSTGLREAEIEAVEVELGRFRDQQYEMLKRWRQQQPAGLGAVYAALE
RWGLDGCVEDLRSTGRFRAGTGRFRDQYEWLKRWRQQQPAGLGAVYAALE
A 496 C 470 G 282 t
         /codon_start=3
/product="death domain receptor 3"
/db_xref="PID:31800293"
/tb_xref="PID:31800293"
/translation="GCAAVAAALLIVILGARAQGGTRSPRCDCAGDFHRKIGIFCCRG
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N71143"
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Number
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                                                                                                                             Length 1528;
GenBank Accession
                                                                                                                                              Indels
                                                                                                                            Score 1511; DB 22;
Pred. No. 0.00e+00;
0; Mismatches 4;
clone 298913,
                                                                                                                              81.8%;
Llarity 99.7%;
Conservative
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Eukaryočae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Bodner, J.L., Burns, K., Schneider, P., Hofmann, K., Steiner, V.,
Thome, M., Bornand, I., Hahne, M., Schroter, M., Wilson, A.,
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                                                                                                                      TGGAGATCGGCCGCTTCCGAGACCAGCAGTACGAGATGCTCAAGCGCTGGCGCCAGCAGC
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                                                                                   ACAGCAGTGAGAAGATCTGCACCGTCCAGTTGGTGGGTAACAGCTGGACCCCTGGCTACC
                                   GAGCICITGGCCCCGCTGCTGCGCCCACACTCTCGCCAGAGTCCCCAGCCGGCTCGCCAG
                        CCGAGACCCAGGAGGCGCTCTGCCCGCAGGTGACATGGTCCTGGGACCAGTTGCCCAGCA
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Human apoptosis-mediating receptor TRAMP mRNA, partial
U75380
91695924
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Immunity 6 (1), 79-88
97205335
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/db_xref="PlD:g1695925"
/translation="AAAGCARYAAALLIVILGARAQGGTRSPRCDCAGDFHKKIGLFC
/translation="AAAGCARYAAALLIVILGARAQGGTRSPRCDCAGDEGASQVALE
CRGPAGHYLKAPCTEPCGARYACGAYAAALLIVILGARBHHHISECARCGACDEGASQVALE
RCGPAGHYRCGGRERYECGYYGGCYSESPFYCQPCLDCGALHRHTRLLCSRRDTDG
TCLLGFYBHGDGCYSCPTSTLGSCPERCAAVGGRYGWYGYYGLAGGYYLLAGTLATU
YTRKGWPHRPLYTADDAGMEALTPPPATHLSPLOSAHTLLAPPDSSEXICTYGLYGATU
SFTPGFALCOPYTWSWDQLPSRALGPPAAPTLSPESPAGSPAMMLQPGPQLYD
VMDAVPARRWKEEVRTGLREBEIEAVEVEIGRFRDQYEMLKRRRQQOPAGLGAVYA
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French, L.E., Browning, J.L., MacDonald, R. and Tschopp, J. Direct Submission Submitted (18-007-1996) Institute of Blochemistry, University Lausanne, 155 Chemin des Boveresses, Epalinges, CH 1066, Switzerland
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Pred. No. 0.00e+00;
0; Mismatches 6; Indels 1;
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                                                                                                              /function="activates NF-kB"
/function="mediates apoptosis"
/note="contains a death domain; similar
/codon_start==
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                                             location/Qualifiers
1. 1557
/ofganism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="fetal lung"
/chromosome="1"
/map="1p36.2"
                                                                                                                                                                                                                                  286
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508 c 477 g 2
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larity 99.5%;
Conservative
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Matches 1520; Conser
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complete cds.
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                                   CTCGCCAGCCATGATGCTGCAGCCGGGCCCGCAGCTCTACGACGTGATGGACGCGGTCCC
                                                     CCAGGIGCICCIGGCIGGCCIIGIGGICCCCCCTCCIGCTIGGGGCCACCCIGACCIACAC
    ATACCGCCACTGCTGGCTCACAAGCCCCTGGTTACTGCAGATGAAGCTGGGATGGAGGC
                                                                                                                                                                                                                                                                                                       1669 bp mRNA PRI
death receptor 3 beta (DR3) mRNA,
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Homo sapiens c
AF026070
g2570830
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RESULT
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To calls to chemotherapeutic drugs or radiation or Example 4; Column 41-46; 54pp; English.

Novel yeast checkpoint control genes Rahli, RAD24, MEC1, MEC2 and Novel yeast checkpoint control genes are responsible for recognising the cell has suffered but damage in the form of radiation or chemical damage or if the cell has failed to complete but chemical damage of chemical inhibition or intrinsic error.

To prior inhibiting mitosis. The purpose of this checkpoint control is that it preserves the viability of the cell and the integrity is that it preserves the viability of the cell and the integrity of the genome by providing the cell time to repair these insults of the genome by providing the cell time to repair these insults or prior to undertaking mitosis. The genes are potentially useful in prior to undertaking mitosis, cancer chemoprevention

Cheveloping cancer chemotherapeutics, cancer chemoprevention

School the genome of the column of the cell and the column of the cell and the chemoprevention or an environmental toxicology tests. They can be used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleotide sequence capable of hybridising with hucDC34 - which is
                                                                                                                                                                                                                                                                                                                     Disclosure; Page 41; 57pp; English.
Disclosure; Page 41; 57pp; English.
The DNA encodes Max-interacting (Mxi) protein-2. Detection of Mxi
gene expression can be used to detect malignant cells in biological
gene expression can be used to detect malignant cells in biological
samples. The Mxi protein-2 and sense/antisense RNA can be delivered
to e.g. bone marrow as therapeutic agents for cancer.
Sequence 1200 BP; 306 A; 270 C; 325 G; 299 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                  Max interacting polypeptide and DNA encoding them - used as anticancer agents and to screen for agents which inhibit cellular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 75; DB 12; Length 1200;
Pred. No. 1.73e-24;
0; Mismatches 0; Indels
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Yeast checkpoint control gene RAD17 cDNA.
RAD17; cell cycle; checkpoint gene; yeast; DNA damage;
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P-PSDB: W26661.
/note- "Max-interacting protein-2"
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12-MAY-1993; WO-U04458.
(HUTC) HUTCHINSON CANCER RES CENT FRED.
(UTAR-) UNIV ARIZONA.
(UNIW ) UNIV WASHINGTON.
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T91037 standard; cDNA to mRNA; 2150 BP.
T91037;
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Query Match
Best Local Similarity 100.0%;
Matches 75; Conservative
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                                                                                                                           29-JAN-1993; US-011398.
(GEHO ) GEN HOSPITAL GORP.
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04-AUG-1994.
29-DEC-1993; U12643.
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WPI; 94-264033/32.
P-PSDB; R56543.
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12-MRR-1993; FR0-248.

12-MRR-1992; FR-003034.

13-MRR-1992; FR-003034.

13-MRR-1992; FR-003034.

13-MRR-1992; FR-003034.

13-MRR-1992; FR-003034.

13-MRR-1992; FR-003034.

13-MRR-1992; FR-003034.

14-Maguin E;

15-MRA-1992; FR-0034.

15-MRR-1992; FR-0034.

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                                                                                                                                                                                                                                                                                                                                                  plasmid pd+host4 containing Ts replication system.
Temperature sensitive replication; antibiotic resistance marker gene;
site-specific recombination; chromosomal integration; inactivation;
heterologous gene expression; thermosensitive plasmid; ds.
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chemical agents that would interfere with checkpoint controls. Cloned genes can also be used to develop yeast strains in which these genes are deleted. Such yeast strains can then be used to find the homologous human genes (see T91034-36). Sequence 2150 BP; 748 Å; 372 C; 425 G; 605 T;
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Q48463;
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Fax: 314 286 1810
Email: estéwatson.wustl.edu
This clone is available royalty-free through LiNL; contact the
This clone is available royalty-free through LiNL;
IMAGE Consortium (info@image.llnl.gov) for further information.
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -41ml3 fwd. Er from Amersham
Seq primer: sequence stop: 253.
High quality sequence stop: 253.
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/clone_lib="Soares total fetus Nb2HF8 9w"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
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(Z .. ص Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Gnathostomata; Osteichthyes; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Theria; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 468)
1 (bases 1.c. Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hallier, L., Clark, N., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., and Thewasis, E., Waterston, R., Williamson, A., Wohldmann, P. and aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, 217 GICTAGGCAIGGIIGGICAGIAGAAGGGIGAACIGCIGACAGACINGGCIGACCINFGCA 276 Washby-Marck EST Project
Washby-Marck EST Project
Washby-Marck EST Project
Washbry to University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson. 277 CICCACAAACCAGCCIGGCIIACAGCCACAGGGGIPICNGCCACINCIGAACAGIICIC 336 548 2182d08.rl Stratagene colon (#937204) Homo sapiens cDNA clone 511119 5', mRNA sequence. 24-OCT-1996 97 CGTGGGGCAGGNACACGGCAGCCATGTTCATAGNAAGNCCAGGCAGGCAGGNTC 156 Gaps . 6 Length 468; 397 GITGITCTCCCAGGCCAAGNAGGTTATITTGGGACACACAAGGCAGGT 444 Score 259; DB 18; Length 466
Pred. No. 0.00e+00;

9: Wismatches 17; Indels others ų 91 /organism="Homo sapiens" /clone="177709" 144 c 118 q 91 Location/Qualifiers The WashU-Merck EST Project midbrain, pons and medulia. Homo sapiens 14.0%; Best Local Similarity 92.5%; Matches 322; Conservative Unpublished (1995) g1633888 ๙ Wilson, R RESULT 13 DEFINITION source ACCESSION BASE COUNT ORGANISM JOURNAL REFERENCE AUTHORS FEATURES ORIGIN TITLE COMMENT გ g ď g g გ S ద გ ე g

KEYWORDS

31-JUL-1995

EST 46374 468 bp mRNA EST yol2d07.rl Homo sapiens cDNA clone 177709 5' H46374.

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human. BASE COUNT 11 FEATURES DEFINITION SOURCE ORGANISM ORIGIN ACCESSION TITLE JOURNAL COMMENT REFERENCE AUTHORS KEYWORDS RESULT ద đ S g Cp ద S d S g ů 7; 1050 GCACCGTCCAGTTGGTGGGTAACAGCTGGACCCTGGCTACCCCGAGACCCAGAGGGGC 1109 1110 TCTGCCCGCAGGTGACATGGTCCTGGGACCAGTTGCCCAGCAGCAGTTTGGCCCCGCTG 1169 TGTCACCCTTGGACAGCGCCCACACCCTTCTAGCACCTCCTGACAGCAGTGAGAAGATCT 126 127 GCACCGTCCAGTTGGTGGGTAACAGCTGGACCCCTGGCTACCCCGAGACCCAGGAGGGG 186 7 CCCTGGTTACTGCAGATGAAGCTGGGATGGAGGCTCTGACCCCACCACCGGCCACCGATC 66 244 CIGCGCCCACACICICGCCAGAGICCCCAGCCGGCTCGCCAAIGANIGCIGCAGCC 303 Eukaryotae: Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Gsteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 443)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and 187 TCTGCC-GCANGTGACATGGTCCTGGGAC-AGTTGCCCAGCAGAN-TCTTGGCCCCGGTG 7; 1228 GGGCCCGCAGCTCTACGACGTGA-TGGACGCGGTCCCA-GCGCGGCGCTCGAA 1278 304 GGGCCCGCAGCTCTACGACGTGAATGGACGCGGTCCCAAGCGCGGCGCTGGAA 356 Length 372; /clone_lib="Soares fetal heart NDHH19w"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="bH10B (ampicillin resistant)"
<1. .>372
133 c 106 g 59 t 3 others 2; Indels H46211 443 bp mRNA EST Yo14h09.rl Homo sapiens CDNA clone 177953 5' Score 302; DB 22; Pred. No. 0.00e+00; 0; Mismatches Wilson, R. The Washu-Merck EST Project Best Local Similarity 97.5%; Matches 344; Conservative ø Query Match mRNA BASE COUNT ORIGIN 10 OCUS DEFINITION CCESSION ID EYWORDS RGANISM ERENCE UTHORS TTLE ô a

Gaps 10; This clone is available royalty-free through LLNL; contact the IMAGE Consortium (life@image.llnl.gov) for further information. 210 GGCATGGTTGGCAGTAGAAGGGTGAACTGCTGACACAGGGTGACCTGGGCACTCCACA 269 270 AACCAGCCTGGCTTACAGCCACAGGGGTT-TCGGCCACTGCTGAACAGTTCTCCAGGGGC 328 329 ACCTGGGNAGGCCTGCTCATTCACAGGCCTGGGCAGCGGGGCACATTTCAGAATTAINGT 388 AA476749, 317 bp mRNA EST 08-AUG-1997 2w94b12.\$1 Soares total fetus Nb2HF8 9w Homo sapiens CDNA clone 7846073', mRNA sequence. Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 317)
H11ller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., White,Y., Wylie,T., Waterston,R., Tan,F., Theising,B., WashU-Merck EST Project 1997 ' Score 269; DB 18; Lengla...
'No. 0.00e+00;
'hes 5; Indels 10; Gz 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Fax: 314 286 1800 Email: estéwatson.wustl.edu High quality sequence stops: 307 Source: IMAGE Consortium, LINL Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 485 GGTTCT-CCCAGGCCAAGAAGGTGTCTT-GGGGACACACACAAGGCAGGT 440 GGTTTTTCCCAGGCCAAGAAGGTTTCTTTGGGGACACACAAGGCAGGT 436 Contact: Wilson RK Washu Merck EST Project Washington University School of Medicine ų 82 /organism="Homo sapiens" /clone="177953" | 138 c 125 g 8: 125 g 14.6%; llarity 95.7%; Conservative Unpublished (1995) Contact: Wilson RK Query Match Best Local Similarity 9 Homo sapiens 93

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ZIP: 20005-3934
COMPUTER READABLE FORM:
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/cgnl_7/ptodata/1/laa/PCTUS_COMB.pep:*
/cgnl_7/ptodata/1/laa/backfiles1.pep:*
GenCore version 4:5
Copyright (c) 1993 - 2000 Compugen Ltd.
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PAPLICANT: 10. (615)402.

APPLICANT: 11. Guo-Liang
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                                                        Gaps
                                          MEQRPRGCAAVAAALLLVILGARAQGGTRSPRCDCAGDFHKKIGLFCCRGCPAGHYLKAP '60
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       Length 417;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     I: Dillon, Patrick J.
INVENTION: Death Domain Containing Receptors
    ; Score 2323; DB 3;
; Pred. No. 1e-193;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6153402 Yet Assigned
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APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                               2, Application US/08815469
  tch 100.0%; al Similarity 100.0%; 417; Conservative 0
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Gentz, Reiner L.
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Ni, Jian
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Matches 417
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                    1488.0310003/EKS/KRM
                                                                                                                                                                                      Score 2267; DB 3;
Pred. No. 7.5e-189;
                                                                                                                                                                                                                  1; Mismatches
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 428 amino acids
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Best Local Similarity 97.1:
Matches 409; Conservative
                                                                                                                                ) MOLECULE TYPE: protein US-08-815-469-2
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                                                                                                                    TOPOLOGY:
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BEST AVAILABLE COPY

UMBER: US 60/028,711 17-0CT-1996

APPLICATION DATA:

LICATION NUMBER:

US 60/013,285

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APPLICANT: Yu, Guo-Liang
APPLICANT: Ni, Jian
APPLICANT: Ni, Jian
APPLICANT: Office of the containing Receptors
TILLE OF INVENTION: Death Domain Containing Receptors
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C. STREET: 1100 New York Ave., NW, Suite 600 CITY: Washington
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned
FILING DATE: 06-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,711
FILING DATE: 17-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY AGENT INFORMATION:
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
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REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMNUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: OF COMPATIBLE
COMP
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LENGTH: 1783 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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4573.803 Million cell updates/sec
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/cgnl_7/ptodata/1/ina/5B_COMB.seq:*
/cgnl_7/ptodata/1/ina/6_COMB.seq:*
/cgnl_7/ptodata/1/ina/PcTUS_COMB.seq:*
/cgnl_7/ptodata/1/ina/backfilesl.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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                                        Length 1783;
                                       Score 1495; DB 3;
Pred. No. 1.3e-299;
0; Mismatches 10;
                                       80.9%;
99.3%;
                                                        Conservative
 CDS 198..1481
                                       Query Match
Best Local Similarity
Matches 1501; Conserv
) NAME/KEY:
; LOCATION:
US-08-815-469-1
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APPLICANT: Ni, Jian
APPLICANT: Dixit, Vishva
APPLICANT: Dixit, Vishva
APPLICANT: Gentz, Reiner L.
APPLICANT: Dillon, Patrick J.
TITLE OF INVENTION: Death Domain Containing Rec
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler C. STREET: 1100 Nover Containing Nov
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: No. 6153402 Yet Assigned FILING DATE: 06-FEB-1997
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APPLICATION NUMBER: US/08/815,469
FILING DATE: HEREWITH
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1 0 ...
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               FILING DATE: 17-007-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,285
FILING DATE: 12-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SFEIF, ELIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0310003/EKS/KRM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 11-02400
TELEFAX: 202-371-2540
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                                                                                                                                                                                                                                                          Score 1254; DB 3;
Pred. No. 5e-250;
0; Mismatches 0;
         UMBER: US 60/028,711
17-OCT-1996
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100.0%; Pre
                                                                                                             INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: ENGINE: 1254 base pairs TYPE: nucleic acid
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PRIOR APPLICATION DATA APPLICATION NUMBER:
                                                                                                                                                                                        MOLECULE TYPE: CDNA
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                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: 1..1
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